



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/708,953  
Source: OIPF  
Date Processed by STIC: 4-5-04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT**

**MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

***Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221***

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

# Raw Sequence Listing Error Summary

Does Not Comply  
Corrected Diskette Needed

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/708,953

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 ☐ Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 ☐ Variable Length     Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 ☐ Skipped Sequences  
    (OLD RULES)     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 ☐ Skipped Sequences  
    (NEW RULES)     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9 ☒ Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 ☐ Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>     Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid

CRFI



Does Not Comply  
Corrected Diskette Needed

IFWO

## RAW SEQUENCE LISTING

DATE: 04/05/2004

PATENT APPLICATION: US/10/708,953

TIME: 14:44:28

Input Set : N:\efs\10708953\_efs\SEQ\_LIST.txt

Output Set: N:\CRF4\04052004\J708953.raw

3 <110> APPLICANT: ROSETTA GENOMICS LTD  
 5 <120> TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY  
 6 OLIGONUCLEOTIDES AND USES THEREOF  
 8 <130> FILE REFERENCE: 55036  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/708,953  
 C--> 10 <141> CURRENT FILING DATE: 2004-04-02  
 10 <160> NUMBER OF SEQ ID NOS: 2254510  
 12 <170> SOFTWARE: PatentIn version 3.2

## ERRORED SEQUENCES

7978577 <210> SEQ ID NO: 886508  
 7978578 <211> LENGTH: 23  
 7978579 <212> TYPE: RNA  
 7978580 <213> ORGANISM: Homo sapiens  
 7978582 <400> SEQUENCE: 886508  
 E--> 7978583 acccag~~g~~gg ggcgcgcugg aca  
 8809835 <210> SEQ ID NO: 978870  
 8809836 <211> LENGTH: 23  
 8809837 <212> TYPE: RNA  
 8809838 <213> ORGANISM: Homo sapiens  
 8809840 <400> SEQUENCE: 978870  
 E--> 8809841 acccag~~g~~gg ggcgcgcugg aca  
 9737897 <210> SEQ ID NO: 1081988  
 9737898 <211> LENGTH: 23  
 9737899 <212> TYPE: RNA  
 9737900 <213> ORGANISM: Homo sapiens  
 9737902 <400> SEQUENCE: 1081988  
 E--> 9737903 acccag~~g~~gg ggcgcgcugg aca  
 9991670 <210> SEQ ID NO: 1110185  
 9991671 <211> LENGTH: 23  
 9991672 <212> TYPE: RNA  
 9991673 <213> ORGANISM: Homo sapiens  
 9991675 <400> SEQUENCE: 1110185  
 E--> 9991676 acccag~~g~~gg ggcgcgcugg aca  
 12803288 <210> SEQ ID NO: 1422587  
 12803289 <211> LENGTH: 23  
 12803290 <212> TYPE: RNA  
 12803291 <213> ORGANISM: Homo sapiens  
 12803293 <400> SEQUENCE: 1422587  
 E--> 12803294 acccag~~g~~gg ggcgcgcugg aca  
 18159737 <210> SEQ ID NO: 2017748

*A feature <220>-<221> is mandatory when 'n' is used as a nucleotide designator. Please see item # 9 on Error Summary Sheet.*

*Same*

*Same*

*Same*

*Same*

23

23

23

23

## RAW SEQUENCE LISTING

DATE: 04/05/2004

PATENT APPLICATION: US/10/708,953

TIME: 14:57:20

Input Set : N:\efs\10708953\_efs\SEQ\_LIST.txt

Output Set: N:\CRF4\04052004\J708953.raw

18159738 &lt;211&gt; LENGTH: 23

18159739 &lt;212&gt; TYPE: RNA

18159740 &lt;213&gt; ORGANISM: Homo sapiens

18159742 &lt;400&gt; SEQUENCE: 2017748

E-->18159743 acccag~~h~~agg gcgucgcugg aca*Same*

23

## VARIABLE LOCATION SUMMARY

DATE: 04/05/2004

PATENT APPLICATION: US/10/708,953

TIME: 14:59:13

Input Set : N:\efs\10708953\_efs\SEQ\_LIST.txt

Output Set: N:\CRF4\04052004\J708953.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:886508; N Pos. 7

Seq#:978870; N Pos. 7

Seq#:1081988; N Pos. 7

Seq#:1110185; N Pos. 7

Seq#:1422587; N Pos. 7

Seq#:2017748; N Pos. 7

## VERIFICATION SUMMARY

DATE: 04/05/2004

PATENT APPLICATION: US/10/708,953

TIME: 14:59:13

Input Set : N:\efs\10708953\_efs\SEQ\_LIST.txt

Output Set: N:\CRF4\04052004\J708953.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:7978583 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:886508

L:8809841 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:978870

L:9737903 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1081988

L:9991676 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1110185

L:12803294 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1422587

L:18159743 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2017748